



BEFORE THE BOARD OF APPEALS AND INTERFERENCES
IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

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1646

In re application of: Baichwal et al.

Group Art Unit: 1646

Serial No. 09/758,003

Examiner: Andres, Janet

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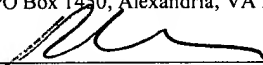
Attorney Docket No. T95-006-2

For: *RIP: Human Protein Involved in
Tumor Necrosis Factor Signal
Transduction*

CERTIFICATE OF MAILING

I hereby certify that this corr. is being deposited with the US Postal Service as First Class Mail in an envelope addressed to the Comm. for Patents, PO Box 1450, Alexandria, VA 22313-1450 on May 20, 2004.

Signed


Richard Osman

BRIEF ON APPEAL

The Honorable Board of Appeals and Interferences
United States Patent and Trademark Office
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Honorable Board:

This is an appeal from the Feb 17, 2004 final rejection of claims 1, 3, 5, 6, 10-27 & 29-34.

REAL PARTY IN INTEREST

The real party in interest is Tularik Inc., which is currently being acquired by Amgen Inc.

RELATED APPEALS AND INTERFERENCES

Appellants are unaware of any related appeals or interferences.

STATUS OF THE CLAIMS

Claims 1, 3, 5, 6, and 10-35 are pending. Claims 28 and 35 are objected to for dependency on a rejected claim. Hence, claims 1, 3, 5, 6, 10-27 and 29-34 are subject to this appeal. Note that the Feb 17, 2004 Action Summary page contains a typographical error

misidentifying the objected to claims as 28 and 34.

STATUS OF THE AMENDMENTS

All Amendments are believed to be properly before the Board.

SUMMARY OF THE INVENTION

Tumor necrosis factor (TNF) is an important cytokine involved in the signaling of a number of cellular responses including cytotoxicity, anti-viral activity, immun.-regulatory activities and the transcriptional regulation of a number of genes. Accordingly, it is desired to identify agents which specifically modulate transduction of TNF receptor family signaling. Specification, p.1, lines 14-23.

The invention provides methods and compositions relating to a human Receptor Interacting Protein (hRIP). Specification, p.2, lines 10-11. hRIP a novel human kinase involved in tumor necrosis factor signal transduction and useful in drug screening. Specification, p.1, lines 10-11.

In a claimed, particular embodiment, the invention provides recombinant RIP-Thr⁵¹⁴ polynucleotides encoding a RIP-Thr⁵¹⁴ polypeptide comprising at least 10 consecutive amino acid residues of SEQ ID NO:2, which consecutive amino acid residues comprise the amino acid residue 514 (Thr) of SEQ ID NO:2, wherein the polypeptide is immunologically distinguishable from RIP-Ser⁵¹⁴. Specification, p.3, lines 13-18; claim 1. Exemplary RIP-Thr⁵¹⁴ polypeptides having RIP-Thr⁵¹⁴ binding specificity and immunologically distinguishable from RIP-Ser⁵¹⁴ are shown in Table I. Specification, p.3, lines 19-31.

In another claimed, particular embodiment, the invention provides isolated or recombinant RIP-ACA¹⁵⁴⁰⁻¹⁵⁴² nucleic acids comprising at least 24 consecutive nucleotides of SEQ ID NO:1, which consecutive nucleotides comprise nucleotides 1540-1542 (ACA) of SEQ ID NO:1, wherein the nucleic acid hybridizes with RIP-ACA¹⁵⁴⁰⁻¹⁵⁴² cDNA but not with RIP-TCT¹⁵⁴⁰⁻¹⁵⁴² cDNA. Specification, p.4, lines 1-4; claim 3. Exemplary RIP-ACA¹⁵⁴⁰⁻¹⁵⁴²

polynucleotides and allele specific oligonucleotide probes having RIP-ACA¹⁵⁴⁰⁻¹⁵⁴² binding specificity and distinguishable by hybridization assays from RIP-TCT¹⁵⁴⁰⁻¹⁵⁴² are shown in Table II. Specification, p.4, lines 4-24.

ISSUES

- I. WHETHER THE EXAMINER'S REJECTION OF CLAIMS 1, 3, 5, 6, 10-27 and 29-34 UNDER 35USC112, FIRST PARAGRAPH (WRITTEN DESCRIPTION) IS CORRECT.
- II. WHETHER THE EXAMINER'S REJECTION OF CLAIMS 1, 3, 5, 6, 10-27 and 29-34 UNDER 35USC112, FIRST PARAGRAPH (ENABLEMENT) IS CORRECT.

GROUPING OF THE CLAIMS

For Issue I, claims 1, 5 and 6 shall stand as a first group; claim 3 shall stand as a second group; claims 10-27 shall stand as a third group; and claims 29-34 shall stand as a fourth group.

For Issue II, claims 1, 5 and 6 shall stand as a first group; claim 3 shall stand as a second group; claims 10-27 shall stand as a third group; and claims 29-34 shall stand as a fourth group.

ARGUMENT

- I. CLAIMS 1, 3, 5, 6, 10-27 and 29-34 ARE PATENTABLE UNDER 35USC112, FIRST PARAGRAPH (WRITTEN DESCRIPTION)

The subject matter of claims 1, 3, 5-6, 10-27 and 29-34 is described in the Specification pursuant to 35USC112, first paragraph, and we are unable to discern in the Final Action any supported, contrary allegation. The Specification discloses a novel RIP variant, having Thr at position 514. The Specification describes and the pending claims are all properly restricted to probes (or reagents or making probes) which distinguish the novel RIP variant (and its corresponding cDNA) from RIP-Ser⁵¹⁴.

Claims 1, 5 and 6 (and all dependencies of claim 1) all require that the polynucleotide encode a RIP-Thr⁵¹⁴ polypeptide comprising at least 10 consecutive amino acid residues of SEQ ID NO:2, which consecutive residues include residue 514 (Thr). Hence, the required region of

the encoded polypeptide is not “only one amino acid”, but one of the only ten possible decapeptides of SEQ ID NO:2 that includes residue 514 (Thr). In addition, the encoded polypeptide is functionally limited to those immunologically distinguishable from RIP-Ser⁵¹⁴. The Specification describes and exemplifies these recited polynucleotides (e.g. p.3, lines 13-31).

Claim 3 and its dependencies are all structurally limited to a RIP-ACA¹⁵⁴⁰⁻¹⁵⁴² nucleic acid comprising at least 24 consecutive nucleotides of the nucleotide sequence set forth as SEQ ID NO:1, which consecutive nucleotides comprise nucleotides 1540-1542 (ACA) of SEQ ID NO:1. Hence, the required common region is limited to one of the only 22 possible 24-mers that include 1540-1542 (ACA) of SEQ ID NO:1. In addition, the nucleic acid is functionally limited to those which hybridize with RIP-ACA¹⁵⁴⁰⁻¹⁵⁴² cDNA but not with RIP-TCT¹⁵⁴⁰⁻¹⁵⁴² cDNA. The Specification describes and exemplifies these recited polynucleotides (e.g. p.4, lines 1-24).

Claims 10-27 are further limited to polynucleotides encoding a RIP-Thr⁵¹⁴ polypeptide comprising a particularly disclosed RIP-Thr⁵¹⁴ truncation meeting the limitations of claim 1 (i.e. wherein the polypeptide comprises at least 10 consecutive residues of SEQ ID NO:2 which comprise the amino acid residue 514 (Thr), wherein the polypeptide is immunologically distinguishable from RIP-Ser⁵¹⁴). These particular truncations are all specifically described (Specification, p.3, lines 22-31); and hence further remove these claims from the Action’s written description rejection.

Claims 29-34 are further limited to polynucleotides comprising a RIP-ACA¹⁵⁴⁰⁻¹⁵⁴² nucleic acid comprising a particularly disclosed RIP-ACA¹⁵⁴⁰⁻¹⁵⁴² polynucleotide meeting the limitations of claim 3 (i.e. wherein the polynucleotide comprises at least 24 consecutive nucleotides of SEQ ID NO:1 which comprise nucleotides 1540-1542 (ACA)). These particular polynucleotides are all specifically described (Specification, p.4, lines 8-24); and hence further remove these claims from the Action’s written description rejection.

II. CLAIMS 1, 3, 5, 6, 10-27 and 29-34 ARE PATENTABLE UNDER 35USC112, FIRST PARAGRAPH (ENABLEMENT)

Claims 1, 3, 5-6, 10-27 and 29-34 are drawn to properly, separately disclosed polynucleotides. That the Sequence Listing rules permit us to describe these separately disclosed

molecules with reference to a single inclusive SEQ ID NO does not mean that we disclose only a single molecule comprising that inclusive SEQ ID NO.

An enablement rejection requires a showing that one skilled in the art could not practice the invention as claimed without undue experimentation. In their broadest recitations, the claims require use of either (a) a polynucleotide encoding a RIP-Thr⁵¹⁴ polypeptide comprising at least 10 consecutive amino acids of SEQ ID NO:2 which comprise the amino acid residue 514 (Thr) of SEQ ID NO:2, wherein the polypeptide is immunologically distinguishable from RIP-Ser⁵¹⁴; or (b) a RIP-ACA¹⁵⁴⁰⁻¹⁵⁴² nucleic acid comprising at least 24 consecutive nucleotides of SEQ ID NO:1 which comprise nucleotides 1540-1542 (ACA) of SEQ ID NO:1, wherein the nucleic acid hybridizes with RIP-ACA¹⁵⁴⁰⁻¹⁵⁴² cDNA but not with RIP-TCT¹⁵⁴⁰⁻¹⁵⁴² cDNA.

As noted above, with regards to Claim 1, 5 and 6 (and all dependencies of claim 1), there only ten possible decapeptides of SEQ ID NO:2 that includes residue 514 (Thr). In addition, the encoded polypeptide is functionally limited to those immunologically distinguishable from RIP-Ser⁵¹⁴. The Specification describes and exemplifies these recited polynucleotides (e.g. p.3, lines 13-31). Similarly, with regards to claim 3 and its dependencies, there are only 22 possible 24-mers that include 1540-1542 (ACA) of SEQ ID NO:1. In addition, the nucleic acid is functionally limited to those which hybridize with RIP-ACA¹⁵⁴⁰⁻¹⁵⁴² cDNA but not with RIP-TCT¹⁵⁴⁰⁻¹⁵⁴² cDNA. The Specification describes and exemplifies these recited polynucleotides (e.g. p.4, lines 1-24).

Ascertaining whether a given polynucleotide falls within the claim requires no more than determining if one of the ten (or 22 in the case of claim 3) possible sequences are present, and using routine screening to determine if the requisite binding/hybridization function is met.

Note that the claims do not encompass any inoperable embodiments; though the claims would be compliant with the enablement requirement even if there were inoperable embodiments.¹ Furthermore, ascertaining the suitability of any given candidate peptide species is

¹ "It is not a function of the claims to specifically exclude possible inoperative substances", *In re Dinh-Nguyen*, 181USPQ46,48(CCPA 1974); see also, *In re Wands* (8 USPQ2d 1400 (Fed Cir 1988), "Even if we were to accept the PTO's 2.8% success rate, we would not be required to reach a conclusion of undue experimentation"; see also, *Atlas Powder Co.*, 224USPQ409,414 (Fed Cir 1994); and, as noted above, the claims do not even encompass inoperative

well within the bounds of empirical experimentation permitted by the enablement requirement of 35USC112, as defined by applicable Federal Circuit law; see *In re Wands* (8 USPQ2d 1400 (Fed Cir 1988)).²

The empirical experimentation necessary to practice alternative embodiments of our invention is less than that permitted under *Wands*. Substituting and testing alternative sequences in the Specification-taught simple binding or hybridization assays does not approach the experimentation required by *Wands*. Our Specification provides more than sufficient teaching to enable one of ordinary skill in this art to practice the claimed invention without undue experimentation. As the 35USC112-compliant experimentation required to generate and screen monoclonal antibodies per *Wands* in 1980 is more extensive and unpredictable than that required here, our claims are in compliance with the enablement requirement of 35USC112.

The rejection appears premised on our claims' use of the open transition "comprising"; like any "comprising" claim, our claims do not preclude additional elements, such as additional nucleotides, beyond those recited – just as do our claims 28 and 35, deemed allowable by the Examiner.

Claims 10-27 are further limited to polynucleotides encoding a RIP-Thr⁵¹⁴ polypeptide comprising a particularly disclosed RIP-Thr⁵¹⁴ truncation meeting the limitations of claim 1 (i.e.

embodiments.

² In *Wands*, the Federal Circuit held that making and screening monoclonal antibodies, even back in 1980, did not constitute undue experimentation. Consider what is *not* undue experimentation: first, immunize, bleed and immunoassay panels of mice, wherein the immunoassay itself is a binding affinity assay; then, after immunizing and confirming the presence of requisite specific antibodies, practitioners of Wand's invention are faced with the daunting and unpredictable tasks of surgically removing the animal's spleen; separating lymphocytes therefrom; mixing the lymphocytes with myeloma cells; treating the mixture to cause a few of the lymphocytes to fuse with a few myeloma cells; isolating from the enormous number of cells in the mixture hybridoma cells that secrete the desired antibody through a series of screening procedures. The entire post-immunization process through serial cloning takes months. The technical feats involved include aseptic surgery, cell fusions, tissue culture with transformed cells which require special health and environmental safety measures, dilution cloning, usually into a bed of immature thymocytes which again requires further aseptic surgery, radiolabel or enzyme-linked immunoassays of secreted antibody, etc. In fact, the vast majority (>97%) of Wand's efforts to produce the claimed antibodies failed.

wherein the polypeptide comprises at least 10 consecutive residues of SEQ ID NO:2 which comprise the amino acid residue 514 (Thr), wherein the polypeptide is immunologically distinguishable from RIP-Ser⁵¹⁴). These particular truncations are all specifically exemplified (Specification, p.3, lines 22-31); and hence further remove these claims from the Action's enablement rejection.

Claims 29-34 are further limited to polynucleotides comprising a RIP-ACA¹⁵⁴⁰⁻¹⁵⁴² nucleic acid comprising a particularly disclosed RIP-ACA¹⁵⁴⁰⁻¹⁵⁴² polynucleotide meeting the limitations of claim 3 (i.e. wherein the polynucleotide comprises at least 24 consecutive nucleotides of SEQ ID NO:1 which comprise nucleotides 1540-1542 (ACA)). These particular polynucleotides are all specifically exemplified (Specification, p.4, lines 9-24); and hence further remove these claims from the Action's enablement rejection.

Appellants respectfully request reversal of the pending Final Action by the Board of Appeals.

We petition for and authorize charging our Deposit Account No.19-0750 all necessary extensions of time. The Commissioner is authorized to charge any fees or credit any overcharges relating to this communication to our Dep. Acct. No.19-0750 (order T95-006-2).

Respectfully submitted,
SCIENCE & TECHNOLOGY LAW GROUP



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CLAIMS ON APPEAL

1. A recombinant polynucleotide encoding a RIP-Thr⁵¹⁴ polypeptide, said polypeptide comprising at least 10 consecutive amino acid residues of the amino acid sequence set forth as SEQ ID NO:2, which consecutive amino acid residues comprise the amino acid residue 514 (Thr) of SEQ ID NO:2, wherein the polypeptide is immunologically distinguishable from RIP-Ser⁵¹⁴.
2. (Canceled)
3. An isolated or recombinant RIP-ACA¹⁵⁴⁰⁻¹⁵⁴² nucleic acid comprising at least 24 consecutive nucleotides of the nucleotide sequence set forth as SEQ ID NO:1, which consecutive nucleotides comprise nucleotides 1540-1542 (ACA) of SEQ ID NO:1, wherein the nucleic acid hybridizes with RIP-ACA¹⁵⁴⁰⁻¹⁵⁴² cDNA but not with RIP-TCT¹⁵⁴⁰⁻¹⁵⁴² cDNA.
4. (Canceled)
5. An isolated cell comprising a nucleic acid according to claim 1.
6. A method of making an isolated RIP polypeptide, said method comprising steps: introducing a nucleic acid according to claim 1 into an isolated host cell or cellular extract, incubating said host cell or extract under conditions whereby said nucleic acid is expressed as a transcript and said transcript is expressed as a translation product comprising said polypeptide, and isolating said translation product.
- 7-9. (Canceled)
10. A polynucleotide according to claim 1, wherein said consecutive amino acid residues comprise $\alpha\Delta 1$ (SEQ ID NO:2, residues 509-518).
11. A polynucleotide according to claim 1, wherein said consecutive amino acid residues

comprise $\alpha\Delta 2$ (SEQ ID NO:2, residues 514-521).

12. A polynucleotide according to claim 1, wherein said consecutive amino acid residues comprise $\alpha\Delta 3$ (SEQ ID NO:2, residues 506-514).

13. A polynucleotide according to claim 1, wherein said consecutive amino acid residues comprise $\alpha\Delta 4$ (SEQ ID NO:2, residues 504-524).

14. A polynucleotide according to claim 1, wherein said consecutive amino acid residues comprise $\alpha\Delta 5$ (SEQ ID NO:2, residues 498-514).

15. A polynucleotide according to claim 1, wherein said consecutive amino acid residues comprise $\alpha\Delta 6$ (SEQ ID NO:2, residues 514-534).

16. A polynucleotide according to claim 1, wherein said consecutive amino acid residues comprise $\alpha\Delta 7$ (SEQ ID NO:2, residues 513-520).

17. A polynucleotide according to claim 1, wherein said consecutive amino acid residues comprise $\alpha\Delta 8$ (SEQ ID NO:2, residues 508-515).

18. A polynucleotide according to claim 1, wherein said consecutive amino acid residues comprise $\alpha\Delta 9$ (SEQ ID NO:2, residues 512-522).

19. A polynucleotide according to claim 1, wherein said consecutive amino acid residues comprise $\alpha\Delta 10$ (SEQ ID NO:2, residues 423-514).

20. A polynucleotide according to claim 1, wherein said consecutive amino acid residues comprise $\alpha\Delta 11$ (SEQ ID NO:2, residues 423-543).

21. A polynucleotide according to claim 1, wherein said consecutive amino acid residues comprise $\alpha\Delta 12$ (SEQ ID NO:2, residues 423-579).
22. A polynucleotide according to claim 1, wherein said consecutive amino acid residues comprise $\alpha\Delta 13$ (SEQ ID NO:2, residues 423-633).
23. A polynucleotide according to claim 1, wherein said consecutive amino acid residues comprise $\alpha\Delta 14$ (SEQ ID NO:2, residues 423-671).
24. A polynucleotide according to claim 1, wherein said consecutive amino acid residues comprise $\alpha\Delta 15$ (SEQ ID NO:2, residues 514-543).
25. A polynucleotide according to claim 1, wherein said consecutive amino acid residues comprise $\alpha\Delta 16$ (SEQ ID NO:2, residues 514-579).
26. A polynucleotide according to claim 1, wherein said consecutive amino acid residues comprise $\alpha\Delta 17$ (SEQ ID NO:2, residues 514-633).
27. A polynucleotide according to claim 1, wherein said consecutive amino acid residues comprise $\alpha\Delta 18$ (SEQ ID NO:2, residues 514-671).
28. (Objected to only; not on appeal) A polynucleotide according to claim 1, wherein said consecutive amino acid residues comprise SEQ ID NO:2.
29. A nucleic acid according to claim 3 comprising at least 36 consecutive nucleotides of the nucleotide sequence set forth as SEQ ID NO:1, which consecutive nucleotides comprise nucleotides 1540-1542 (ACA) of SEQ ID NO:1.
30. A nucleic acid according to claim 3 comprising at least 48 consecutive nucleotides of the

nucleotide sequence set forth as SEQ ID NO:1, which consecutive nucleotides comprise nucleotides 1540-1542 (ACA) of SEQ ID NO:1.

31. A nucleic acid according to claim 3 comprising at least 72 consecutive nucleotides of the nucleotide sequence set forth as SEQ ID NO:1, which consecutive nucleotides comprise the nucleotides 1540-1542 (ACA) of SEQ ID NO:1.

32. A nucleic acid according to claim 3 comprising at least 148 consecutive nucleotides of the nucleotide sequence set forth as SEQ ID NO:1, which consecutive nucleotides comprise nucleotides 1540-1542 (ACA) of SEQ ID NO:1.

33. A nucleic acid according to claim 3 comprising at least 356 consecutive nucleotides of the nucleotide sequence set forth as SEQ ID NO:1, which consecutive nucleotides comprise nucleotides 1540-1542 (ACA) of SEQ ID NO:1.

34. A nucleic acid according to claim 3, wherein the consecutive nucleotides are selected from the group consisting of nucleotides 1540-1557, 1540-1563, 1540-1675, 1540-1699, 1525-1542, 1519-1542, 1507-1542, 1483-1542, 1537-1545, 1534-1548, 1528-1554, 1516-1566, 1504-1554 and 1492-1568 of SEQ ID NO:1.

35. (Objected to only; not on appeal) A nucleic acid according to claim 3 comprising the nucleotide sequence set forth as SEQ ID NO:1.